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## RAW SEQUENCE LISTING

DATE: 09/13/2001

PATENT APPLICATION: US/09/939,484

TIME: 10:57:52

Input Set : A:\DIV.txt

Output Set: N:\CRF3\09132001\I939484.raw

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3 <110> APPLICANT: Duprat, Fabrice  
 4 Lesage, Florian  
 5 Fink, Michel  
 6 Lazdunski, Michel  
 8 <120> TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR CLONING  
 9 AND THEIR USE, ESPECIALLY FOR THE SCREENING OF DRUGS  
 11 <130> FILE REFERENCE: 1201-CIP-DIV-00  
 W--> 13 <140> CURRENT APPLICATION NUMBER: US/09/939,484  
 13 <141> CURRENT FILING DATE: 2001-08-24  
 15 <150> PRIOR APPLICATION NUMBER: 09/144,914  
 16 <151> PRIOR FILING DATE: 1998-09-01  
 18 <150> PRIOR APPLICATION NUMBER: 08/749,816  
 19 <151> PRIOR FILING DATE: 1996-11-15  
 21 <150> PRIOR APPLICATION NUMBER: 60/095,234  
 22 <151> PRIOR FILING DATE: 1998-08-04  
 24 <150> PRIOR APPLICATION NUMBER: FR 96/01565  
 25 <151> PRIOR FILING DATE: 1996-02-08  
 27 <160> NUMBER OF SEQ ID NOS: 24  
 29 <170> SOFTWARE: PatentIn Ver. 2.0  
 31 <210> SEQ ID NO: 1  
 32 <211> LENGTH: 1894  
 33 <212> TYPE: DNA  
 34 <213> ORGANISM: Homo sapiens  
 36 <220> FEATURE:  
 37 <221> NAME/KEY: CDS  
 38 <222> LOCATION: (183)..(1190)  
 40 <220> FEATURE:  
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 46 gcgggcggga gccaggcccg ggcgggggcg ggggcgggcg ggccagaaga ggcggcgggc 120  
 48 cgcgctcccg ccggtctgcg gcgttggcct tggtttggc tttggcggcg gcggtggaga 180  
 50 ag atg ctg cag tcc ctg gcc ggc agc tcg tgc gtg cgc ctg gtg gag 227  
 51 Met Leu Gln Ser Leu Ala Gly Ser Ser Cys Val Arg Leu Val Glu  
 52 1 5 10 15  
 54 cgg cac cgc tcg gcc tgg tgc ttc ggc ttc ctg gtg ctg ggc tac ttg 275  
 55 Arg His Arg Ser Ala Trp Cys Phe Gly Phe Leu Val Leu Gly Tyr Leu  
 56 20 25 30  
 58 ctc tac ctg gtc ttc ggc gca gtg gtc ttc tcc tcg gtg gag ctg ccc 323  
 59 Leu Tyr Leu Val Phe Gly Ala Val Val Phe Ser Ser Val Glu Leu Pro  
 60 35 40 45  
 62 tat gag gac ctg ctg cgc cag gag ctg cgc aag ctg aag cga cgc ttc 371  
 63 Tyr Glu Asp Leu Leu Arg Gln Glu Leu Arg Lys Leu Lys Arg Arg Phe  
 64 50 55 60  
 66 ttg gag gag cac gag tgc ctg tct gag cag cag ctg gag cag ttc ctg 419  
 67 Leu Glu Glu His Glu Cys Leu Ser Glu Gln Gln Leu Glu Gln Phe Leu  
 68 65 70 75

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70 ggc cgg gtg ctg gag gcc agc aac tac ggc gtg tcg gtg ctc agc aac 467
71 Gly Arg Val Leu Glu Ala Ser Asn Tyr Gly Val Ser Val Leu Ser Asn
72 80 85 90 95
74 gcc tcg ggc aac tgg aac tgg gac ttc acc tcc gcg ctc ttc ttc gcc 515
75 Ala Ser Gly Asn Trp Asn Trp Asp Phe Thr Ser Ala Leu Phe Phe Ala
76 100 105 110
78 agc acc gtg ctc tcc acc aca ggt tat ggc cac acc gtg ccc ttg tca 563
79 Ser Thr Val Leu Ser Thr Thr Gly Tyr Gly His Thr Val Pro Leu Ser
80 115 120 125
82 gat gga ggt aag gcc ttc tgc atc atc tac tcc gtc att ggc att ccc 611
83 Asp Gly Gly Lys Ala Phe Cys Ile Ile Tyr Ser Val Ile Gly Ile Pro
84 130 135 140
86 ttc acc ctc ctg ttc ctg acg gct gtg gtc cag cgc atc acc gtg cac 659
87 Phe Thr Leu Leu Phe Leu Thr Ala Val Val Gln Arg Ile Thr Val His
88 145 150 155
90 gtc acc cgc agg ccg gtc ctc tac ttc cac atc cgc tgg ggc ttc tcc 707
91 Val Thr Arg Arg Pro Val Leu Tyr Phe His Ile Arg Trp Gly Phe Ser
92 160 165 170 175
94 aag cag gtg gtg gcc atc gtc cat gcc gtg ctc ctt ggg ttt gtc act 755
95 Lys Gln Val Val Ala Ile Val His Ala Val Leu Leu Gly Phe Val Thr
96 180 185 190
98 gtg tcc tgc ttc ttc ttc atc ccg gcc gct gtc ttc tca gtc ctg gag 803
99 Val Ser Cys Phe Phe Phe Ile Pro Ala Ala Val Phe Ser Val Leu Glu
100 195 200 205
102 gat gac tgg aac ttc ctg gaa tcc ttt tat ttt tgt ttt att tcc ctg 851
103 Asp Asp Trp Asn Phe Leu Glu Ser Phe Tyr Phe Cys Phe Ile Ser Leu
104 210 215 220
106 agc acc att ggc ctg ggg gat tat gtg cct ggg gaa ggc tac aat caa 899
107 Ser Thr Ile Gly Leu Gly Asp Tyr Val Pro Gly Glu Gly Tyr Asn Gln
108 225 230 235
110 aaa ttc aga gag ctc tat aag att ggg atc acg tgt tac ctg cta ctt 947
111 Lys Phe Arg Glu Leu Tyr Lys Ile Gly Ile Thr Cys Tyr Leu Leu Leu
112 240 245 250 255
114 ggc ctt att gcc atg ttg gta gtt ctg gaa acc ttc tgt gaa ctc cat 995
115 Gly Leu Ile Ala Met Leu Val Val Leu Glu Thr Phe Cys Glu Leu His
116 260 265 270
118 gag ctg aaa aaa ttc aga aaa atg ttc tat gtg aag aag gac aag gac 1043
119 Glu Leu Lys Lys Phe Arg Lys Met Phe Tyr Val Lys Lys Asp Lys Asp
120 275 280 285
122 gag gat cag gtg cac atc ata gag cat gac caa ctg tcc ttc tcc tcg 1091
123 Glu Asp Gln Val His Ile Ile Glu His Asp Gln Leu Ser Phe Ser Ser
124 290 295 300
126 atc aca gac cag gca gct ggc atg aaa gag gac cag aag caa aat gag 1139
127 Ile Thr Asp Gln Ala Ala Gly Met Lys Glu Asp Gln Lys Gln Asn Glu
128 305 310 315
130 cct ttt gtg gcc acc cag tca tct gcc tgc gtg gat ggc cct gca aac 1187
131 Pro Phe Val Ala Thr Ser Ser Ala Cys Val Asp Gly Pro Ala Asn
132 320 325 330 335
134 cat tgagcgtagg atttggtgca ttatgctaga gcaccagggg caggggtgcaa 1240

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135 His
137 ggaagaggct taagtatggt cattttttatc agaatgcaaa agcgaaaatt atgtcacttt 1300
139 aagaaatagc tactgtttgc aatgtcttat taaaaaaciaa caaaaaaaga cacatggaac 1360
141 aaagaagctg tgaccccagc aggatgtcta atatgtgagg aaatgagatg tccacctaaa 1420
143 attcatatgt gacaaaatta tctcgacctt acataggagg agaatacttg aagcagtatg 1480
145 ctgctgtggt tagaagcaga ttttatactt ttaactggaa actttggggt ttgcatttag 1540
147 atcatttagc tgatggctaa atagcaaaat ttatatattag aagcaaaaaa aaaaagcata 1600
149 gagatgtggt ttataaatag gtttatgtgt actggtttgc atgtaccac ccaaatgat 1660
151 tatttttggg gaatctaagt caaactcact atttataatg cataggtaac cattaactat 1720
153 gtacatatata agtataaata tgtttatatatt ctgtacatat ggtttagggtc accagatcct 1780
155 agtgtagtgc tgaaactaag actatagata ttttgtttct tttgatttct ctttatacta 1840
157 aagaatccag agttgctaca ataaaataag gggaataata aaaaaaaaaa aaaa 1894
160 <210> SEQ ID NO: 2
161 <211> LENGTH: 336
162 <212> TYPE: PRT
163 <213> ORGANISM: Homo sapiens
165 <220> FEATURE:
166 <223> OTHER INFORMATION: TWIK-1
168 <400> SEQUENCE: 2
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170 1 5 10 15
172 His Arg Ser Ala Trp Cys Phe Gly Phe Leu Val Leu Gly Tyr Leu Leu
173 20 25 30
175 Tyr Leu Val Phe Gly Ala Val Val Phe Ser Ser Val Glu Leu Pro Tyr
176 35 40 45
178 Glu Asp Leu Leu Arg Gln Glu Leu Arg Lys Leu Lys Arg Arg Phe Leu
179 50 55 60
181 Glu Glu His Glu Cys Leu Ser Glu Gln Gln Leu Glu Gln Phe Leu Gly
182 65 70 75 80
184 Arg Val Leu Glu Ala Ser Asn Tyr Gly Val Ser Val Leu Ser Asn Ala
185 85 90 95
187 Ser Gly Asn Trp Asn Trp Asp Phe Thr Ser Ala Leu Phe Phe Ala Ser
188 100 105 110
190 Thr Val Leu Ser Thr Thr Gly Tyr Gly His Thr Val Pro Leu Ser Asp
191 115 120 125
193 Gly Gly Lys Ala Phe Cys Ile Ile Tyr Ser Val Ile Gly Ile Pro Phe
194 130 135 140
196 Thr Leu Leu Phe Leu Thr Ala Val Val Gln Arg Ile Thr Val His Val
197 145 150 155 160
199 Thr Arg Arg Pro Val Leu Tyr Phe His Ile Arg Trp Gly Phe Ser Lys
200 165 170 175
202 Gln Val Val Ala Ile Val His Ala Val Leu Leu Gly Phe Val Thr Val
203 180 185 190
205 Ser Cys Phe Phe Phe Ile Pro Ala Val Phe Ser Val Leu Glu Asp
206 195 200 205
208 Asp Trp Asn Phe Leu Glu Ser Phe Tyr Phe Cys Phe Ile Ser Leu Ser
209 210 215 220
211 Thr Ile Gly Leu Gly Asp Tyr Val Pro Gly Glu Gly Tyr Asn Gln Lys
212 225 230 235 240

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214 Phe Arg Glu Leu Tyr Lys Ile Gly Ile Thr Cys Tyr Leu Leu Leu Gly
215                245                250                255
217 Leu Ile Ala Met Leu Val Val Leu Glu Thr Phe Cys Glu Leu His Glu
218                260                265                270
220 Leu Lys Lys Phe Arg Lys Met Phe Tyr Val Lys Lys Asp Lys Asp Glu
221                275                280                285
223 Asp Gln Val His Ile Ile Glu His Asp Gln Leu Ser Phe Ser Ser Ile
224                290                295                300
226 Thr Asp Gln Ala Ala Gly Met Lys Glu Asp Gln Lys Gln Asn Glu Pro
227 305                310                315                320
229 Phe Val Ala Thr Gln Ser Ser Ala Cys Val Asp Gly Pro Ala Asn His
230                325                330                335
233 <210> SEQ ID NO: 3
234 <211> LENGTH: 2514
235 <212> TYPE: DNA
236 <213> ORGANISM: Homo sapiens
238 <220> FEATURE:
239 <221> NAME/KEY: CDS
240 <222> LOCATION: (126)..(1307)
242 <220> FEATURE:
243 <223> OTHER INFORMATION: TASK
245 <400> SEQUENCE: 3
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248 gcggcgcccg gggccgatgc gcgggccggg ggcgcggggg ggccggcggc ggcccgggcg 120
250 ggacg atg aag cgg cag aac gtg cgc acg ctg gcg ctc atc gtg tgc acc 170
251 Met Lys Arg Gln Asn Val Arg Thr Leu Ala Leu Ile Val Cys Thr
252 1 5 10 15
254 ttc acc tac ctg ctg gtg ggc gcc gcg gtc ttc gac gcg ctg gag tgc 218
255 Phe Thr Tyr Leu Leu Val Gly Ala Ala Val Phe Asp Ala Leu Glu Ser
256 20 25 30
258 gag ccc gag ctg atc gag cgg cag cgg ctg gag ctg cgg cag cag gag 266
259 Glu Pro Glu Leu Ile Glu Arg Gln Arg Leu Glu Leu Arg Gln Gln Glu
260 35 40 45
262 ctg cgg gcg cgc tac aac ctc agc cag ggc ggc tac gag gag ctg gag 314
263 Leu Arg Ala Arg Tyr Asn Leu Ser Gln Gly Gly Tyr Glu Glu Leu Glu
264 50 55 60
266 cgc gtc gtg ctg cgc ctc aag ccg cac aag gcc ggc gtg cag tgg cgc 362
267 Arg Val Val Leu Arg Leu Lys Pro His Lys Ala Gly Val Gln Trp Arg
268 65 70 75
270 ttc gcc ggc tcc ttc tac ttc gcc atc acc gtc atc acc acc atc ggc 410
271 Phe Ala Gly Ser Phe Tyr Phe Ala Ile Thr Val Ile Thr Thr Ile Gly
272 80 85 90 95
274 tac ggg cac gcg gca ccc agc acg gat ggc ggc aag gtg ttc tgc atg 458
275 Tyr Gly His Ala Ala Pro Ser Thr Asp Gly Gly Lys Val Phe Cys Met
276 100 105 110
278 ttc tac gcg ctg ctg ggc atc ccg ctc acg ctc gtc atg ttc cag agc 506
279 Phe Tyr Ala Leu Leu Gly Ile Pro Leu Thr Leu Val Met Phe Gln Ser
280 115 120 125
282 ctg ggc gag cgc atc aac acc ttg gtg agg tac ctg ctg cac cgc gcc 554

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283 Leu Gly Glu Arg Ile Asn Thr Leu Val Arg Tyr Leu Leu His Arg Ala
284      130      135      140
286 aag aag ggg ctg ggc atg cgg cgc gcc gac gtg tcc atg gcc aac atg 602
287 Lys Lys Gly Leu Gly Met Arg Arg Ala Asp Val Ser Met Ala Asn Met
288      145      150      155
290 gtg ctc atc ggc ttc ttc tcg tgc atc agc acg ctg tgc atc ggc gcc 650
291 Val Leu Ile Gly Phe Phe Ser Cys Ile Ser Thr Leu Cys Ile Gly Ala
292 160      165      170      175
294 gcc gcc ttc tcc cac tac gag cac tgg acc ttc ttc cag gcc tac tac 698
295 Ala Ala Phe Ser His Tyr Glu His Trp Thr Phe Phe Gln Ala Tyr Tyr
296      180      185      190
298 tac tgc ttc atc acc ctc acc acc atc ggc ttc ggc gac tac gtg gcg 746
299 Tyr Cys Phe Ile Thr Leu Thr Thr Ile Gly Phe Gly Asp Tyr Val Ala
300      195      200      205
302 ctg cag aag gac cag gcc ctg cag acg cag ccg cag tac gtg gcc ttc 794
303 Leu Gln Lys Asp Gln Ala Leu Gln Thr Gln Pro Gln Tyr Val Ala Phe
304      210      215      220
306 agc ttc gtc tac atc ctt acg ggc ctc acg gtc atc ggc gcc ttc ctc 842
307 Ser Phe Val Tyr Ile Leu Thr Gly Leu Thr Val Ile Gly Ala Phe Leu
308      225      230      235
310 aac ctc gtg gtg ctg cgc ttc atg acc atg aac gcc gag gac gag aag 890
311 Asn Leu Val Val Leu Arg Phe Met Thr Met Asn Ala Glu Asp Glu Lys
312 240      245      250      255
314 cgc gac gcc gag cac cgc gcg ctg ctc acg cgc aac ggg cag gcg ggc 938
315 Arg Asp Ala Glu His Arg Ala Leu Leu Thr Arg Asn Gly Gln Ala Gly
316      260      265      270
318 ggc ggc gga ggg ggt ggc agc gcg cac act acg gac acc gcc tca tcc 986
319 Gly Gly Gly Gly Gly Ser Ala His Thr Thr Asp Thr Ala Ser Ser
320      275      280      285
322 acg gcg gca gcg ggc ggc ggc ggc ttc cgc aac gtc tac gcg gag gtg 1034
323 Thr Ala Ala Ala Gly Gly Gly Gly Phe Arg Asn Val Tyr Ala Glu Val
324      290      295      300
326 ctg cac ttc cag tcc atg tgc tcg tgc ctg tgg tac aag agc cgc gag 1082
327 Leu His Phe Gln Ser Met Cys Ser Cys Leu Trp Tyr Lys Ser Arg Glu
328      305      310      315
330 aag ctg cag tac tcc atc ccc atg atc atc ccg cgg gac ctc tcc acg 1130
331 Lys Leu Gln Tyr Ser Ile Pro Met Ile Ile Pro Arg Asp Leu Ser Thr
332 320      325      330      335
334 tcc gac acg tgc gtg gag cag agc cac tcg tcg ccg gga ggg ggc ggc 1178
335 Ser Asp Thr Cys Val Glu Gln Ser His Ser Ser Pro Gly Gly Gly Gly
336      340      345      350
338 cgc tac agc gac acg ccc tcg cga cgc tgc ctg tgc agc ggg gcg cca 1226
339 Arg Tyr Ser Asp Thr Pro Ser Arg Arg Cys Leu Cys Ser Gly Ala Pro
340      355      360      365
342 cgc tcc gcc atc agc tcg gtg tcc acg ggt ctg cac agc ctg tcc acc 1274
343 Arg Ser Ala Ile Ser Ser Val Ser Thr Gly Leu His Ser Leu Ser Thr
344      370      375      380
346 ttc cgc ggc ctc atg aag cgc agg agc tcc gtg tgactgcccc gagggacctg 1327
347 Phe Arg Gly Leu Met Lys Arg Arg Ser Ser Val

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VERIFICATION SUMMARY

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